

SEQUENCE PROTOCOL

<110> Degussa-Hüls AG, Forschungszentrum Jülich GmbH

<120> New nucleotide sequences which code for the fadD15 gene

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<170> PatentIn Ver. 2.1

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<213> Corynebacterium glutamicum

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taagaagtta ttgacacact gaatacatag agaaaaattc catgtgggta aagatatgcc 180

taaagatctg accaaaaacg tgactaaaga cgtgacgaca caagtacagc caaattaaag 240

gaaagg ttg aat ttg acc atg act tca cct aat acc ctg cag gaa tac 288

Leu Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr
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act gaa cct gcc aag tac acc atc gga gaa tct gaa acc tgc ctg acc 336

Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr
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gcc ctt cta gat cag att aag act cga cct tac gga gtt ttg ttc agc 384

Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser
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aag cct gcc aac tat gag tgg gtg aat gta act gcc aaa gaa ttt cag 432

Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln
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Asp Glu Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu	
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cag gga gac cgt gtc gcg ctg ctg tcc aat act cgc tat gag tgg gct	528
Gln Gly Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala	
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Val Leu Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile	
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tac agc tcc tct tca ctg tcc caa att gag tgg atc att gag gat tcc	624
Tyr Ser Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser	
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ggc gct gtt ttg gcc att acc gaa acc cct gat cat acc gac ttg atg	672
Gly Ala Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met	
130 135 140	
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Pro Ser Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu	
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Thr Leu Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu	
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Arg Ile His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr	
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Ser Gly Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His	
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Trp Leu Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile	
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Ala Met Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val	
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Ser His Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser	
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530 535 540												
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Glu Ser Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala												
545 550 555												
gaa atc cag gat gca gtc aac aac gct aat gcc acg gtg tct cat tca	1968											

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Glu Ala Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu
575 580 585 590

gcc gac gag ctg acc cca acg ctg aag gtc aag cgc aac gtt gtt gtt 2064
Ala Asp Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val
595 600 605

cgc cgt tac gca gac gcc atc gac cac atc tac aac cga tgagtaacac 2113
Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
610 615

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Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly
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Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser
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Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala
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Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn
130 135 140

Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser
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Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu
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Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp
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 Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile
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 Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
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